

# EXHIBIT A

# Alignment of amino acid sequences of glutaminases

		1	50
gls (2247)	(1)	MVAFESLWPQNLSCTRVYSAKEIISLDSLIMPPEYLHEILDDVRDITS	
GLSA_CORGL	(1)	-----LIMPPEYLHEILDDVRDITS	
GLSA_COREF	(1)	-----MTTHPLIMPPEYFEEILSVRSVS	
GLSA1_BRAJA	(1)	-----TTPPASWTRSKPPLRFIDTCLNFSATIS	
GLSA2_BRAJA	(1)	-----MDTQPIRLPSAGATRSGYPTRPPLRRITICHELFRGDS	
GLSA_ANASP	(1)	-----SDQANQGDLEIRPSPLKVINLHISKYSLKE	
Consensus	(1)	MS SA MLTMPIEYL EILDDVRSDTS	
		51	100
gls (2247)	(51)	GEADYIPELKSAADPNPLAVALCTVNGHYSAGDDDEFTIQSISKPFAY	
GLSA_CORGL	(23)	GEADYIPELKSAADPNPLAVALCTVNGHYSAGDDDEFTIQSISKPFAY	
GLSA_COREF	(27)	GEADYIPELKSAADPNPLAVALCTVDGHYAGDDDEFTIQSISKPFAY	
GLSA1_BRAJA	(33)	GAVADYIPELGNADPAYFGISLATDGHVYEVGDSRPFTIQSISKPFV	
GLSA2_BRAJA	(43)	GEADYIPELKRAIPDHFGIALVTIDGHVYEVGDSAPFTIQSISKAFV	
GLSA_ANASP	(34)	GTIVANYIPELAKVNPDLFSISIVTVDGQVYQVGDYQQLFTIQSISKVFAY	
Consensus	(51)	GEADYIPELKADPNPLAVALCTVDGHIYVGDDDEFTIQSISKPFAY	
		101	150
gls (2247)	(101)	ALALQECGFDEVSAVALEPSGEAFNEISLDG-ENRPMNPMINAGAIAIN	
GLSA_CORGL	(73)	ALALQECGFDEVSAVALEPSGEAFNEISLDG-ENRPMNPMINAGAIAIN	
GLSA_COREF	(77)	ALALQECGPEKVFATVGLEPSGEAFNEISLDGSTNRPMNPMINAGAIAIN	
GLSA1_BRAJA	(83)	ALALDLLGAGRVESAGLEPSGDPFNSRLNSDN-HPFNPMINAGAIACT	
GLSA2_BRAJA	(93)	ALALETVGEERVSATIGLEPSGEAFNSRLINDN-RPFNPMINAGAIACS	
GLSA_ANASP	(84)	GLALEDHGRDYVLRVGVPEGEAFNAIIDEQSKRPYNPMINAGAIATT	
Consensus	(101)	ALALQEGDRVSASVLEPSGEAFNEISLDGNRPMNPMINAGAIAIN	
		151	200
gls (2247)	(150)	QLINGSDSIVEDRVEKIRHYFSELAGRELIDRVLAESLAGADRNLISIA	
GLSA_CORGL	(122)	QLINGSDSIVEDRVEKIRHYFSELAGRELIDRVLAESLAGADRNLISIA	
GLSA_COREF	(127)	QLINGSSESVEDRVEKIRSYFSELAGRELIDRQLSETELEGADRNLISIA	
GLSA1_BRAJA	(132)	GLIYDSKG--AAFEQIRLALSRFAGRDLADEAVSSESQTGDRNRATIG	
GLSA2_BRAJA	(142)	GLIYEVDG--KGAFERRSKLSEFAGRELGVDEAVHASETATGNRNRATIA	
GLSA_ANASP	(134)	SLIKGAG--TERRNLEMFERRYIGHYFDISVFTSERSTIGHNRNAMA	
Consensus	(151)	QLINGSDSIVEDRVEKIRYFSELAGRELIDRALAESLATADRNRATIA	
		201	250
gls (2247)	(200)	HMLRNYGVIEDDAHDAVLSYTLQCAIKVTIRDLAVMTATLAAGGTHPITG	
GLSA_CORGL	(172)	HMLRNYGVIEDDAHDAVLSYTLQCAIKVTIRDLAVMTATLAAGGTHPITG	
GLSA_COREF	(177)	HMLRNYGVIEDDAHDAVLSYTLQCSVKVTARDLAVMTATLAAGGTQPTG	
GLSA1_BRAJA	(180)	YLLKTNVAVSDNVAAVDVYFROCAVLTARDLAVMAATLANRGINPITG	
GLSA2_BRAJA	(190)	YLLRNYAVLPDVDAVDVYFROCAVLTARDLAVMAATLANRGINPITG	
GLSA_ANASP	(182)	YLLNFGMTIRNIEEALDLYFQCCAMYNCHDLAVMAATLANRGVNPITG	
Consensus	(201)	HLLRNYGVIEDDAHDALLSYTLQCAIKVTARDLAVMTATLANRGINPITG	
		251	300
gls (2247)	(250)	KKLDARVRLTSLVMASAGMYDEAGQWLSTVGIPAKSGVAGGIGILPG	
GLSA_CORGL	(222)	KKLDARVRLTSLVMASAGMYDEAGQWLSTVGIPAKSGVAGGIGILPG	
GLSA_COREF	(227)	EKLVDARVARLVLSLTMASAGMYDEAGQWLATVGIPAKSGVSGGLVGVLPG	
GLSA1_BRAJA	(230)	EDVVSAYASRTLSVMTSSGMYDYAGEVYRIGIPAKSGVGGGLAALPA	
GLSA2_BRAJA	(240)	ADVITPHIVARTLSVMTSSGMYDYAGEVYRIGIPAKSGVGGGVAALPS	
GLSA_ANASP	(232)	EQAVNSRYIKDTLSVMTTCGMYNFAGEVAYKVIGIPAKSGVCGGIMAVVPN	
Consensus	(251)	EQLLDARVIRLTSLVMASAGMYDEAGQWLYTVGIPAKSGVAGGIIATLPG	
		301	350
gls (2247)	(300)	QLGIATFSPRLNPKGNSVRGVKIFKALSDDMGLHLMSTEQVSGHAVRSIT	
GLSA_CORGL	(272)	QLGIATFSPRLNPKGNSVRGVKIFKALSDDMGLHLMSTEQVSGHAVRSIT	
GLSA_COREF	(277)	QLGIATFSPRLNSQGNPVRGVEIFKALSDDMGLHLMSEALIQHAVRAIE	
GLSA1_BRAJA	(280)	RLGGSYSPKLDKHGNSVRGKYCEALSSHVDLHMLNRSDDRNAVITADY	
GLSA2_BRAJA	(290)	QLGIATFSPRLDNHNSVRGLKYCEALSARFDLHMLNRNADVRTSMADY	
GLSA_ANASP	(282)	LIGAVFSPPLDIRGNSVRGVKICEELSQLGLHLFECKMVGNGEWGVGN	
Consensus	(301)	QLGIATFSPRLNKGNSVRGVKIFKALSDDMGLHLMSEVS HAVRAI	
		351	400
gls (2247)	(350)	RG-----DTTFIQMGAMNFSAESELHAIVEH	
GLSA_CORGL	(322)	RG-----DTTFIQMGAMNFSAESELHAIVEH	
GLSA_COREF	(327)	RG-----DTTIQLQMGAMNFSAEENELFTITDH	
GLSA1_BRAJA	(330)	DIIGKSPSRVRRAQEREILAAHEQVRIITELVGTSLSAVDYVSRRLAGR	

GLSA2_BRAJA	(340)	IVYGISSRRSRQPHEQQILDERHSDIRVLEVGALNFGTIYVTRRTSE
GLSA_ANASP	(332)	CEC-----
Consensus	(351)	DDG-----DTTIQLQGAMNFSASE FL I EH
		401-----450
gls (2247)	(379)	NFEGTEVVLDTLTVLSFHPVAIRMKEGLKRIRDAGFEVFLDPDDVLPD
GLSA_CORGL	(351)	NFEGTEVVLDTLTVLSFHPVAIRMKEGLKRIRDAGFEVFLDPDDVLPD
GLSA_COREF	(356)	DETGEKVVDLSRVPMFRPMGRRLVKEGLRRI RDNGEKVAIYDPEDILPD
GLSA1_BRAJA	(380)	P-RPQFVFDLHRVTSTTRAGARLYAEAFEEAALNVTVVSGVRRASKE
GLSA2_BRAJA	(390)	PPNAPLIDFRRVPDITAAGAELEGITITAGNANVTTIISGLTASAV
GLSA_ANASP	(335)	-----
Consensus	(401)	F G VVLDLTV SF PVG RLIEGLKRIRDAGF V I DPDDVLPD
		451-----500
gls (2247)	(429)	FMSDGTICKERV-----
GLSA_CORGL	(401)	FMSDGTICKERV-----
GLSA_COREF	(406)	FDFSDGTKSPQVDDPEEL-----
GLSA1_BRAJA	(429)	VNTLREWTAELINVRDFYLLDTAIEWAEDQIVYRYGGSIDFHETTELAEQ
GLSA2_BRAJA	(440)	AAIAARTGDPRLRRFALLDDAIEWAEDQVIYRFGGFTDVKESVHLGEQ
GLSA_ANASP	(335)	-----
Consensus	(451)	F FSDGT R-----
		501-----550
gls (2247)	(442)	-----
GLSA_CORGL	(414)	-----
GLSA_COREF	(424)	-----
GLSA1_BRAJA	(479)	PLLEGLSADELAELGAICTIRTYQSGAKILTTGDPADALFFLRSGAVHVT
GLSA2_BRAJA	(490)	ALLAELDTDEIAAIVKLSTTRHYTAGQRVIAAGAPANSLFFLQSGMVSVK
GLSA_ANASP	(335)	-----
Consensus	(501)	-----
		551-----600
gls (2247)	(442)	-----
GLSA_CORGL	(414)	-----
GLSA_COREF	(424)	-----
GLSA1_BRAJA	(529)	LPDGVRLATLTAGMAFGEMALLEQTRSADVFADMAATAFEAPLKDFERFR
GLSA2_BRAJA	(540)	LRSGVRLASLPGMEFGEMAILERTRSADVFADTPVACLELPLDSFADYR
GLSA_ANASP	(335)	-----
Consensus	(551)	-----
		601-----635
gls (2247)	(442)	-----
GLSA_CORGL	(414)	-----
GLSA_COREF	(424)	-----
GLSA1_BRAJA	(579)	EQHPRASERIMRNLAQLLADRLIVANAKVDILTST
GLSA2_BRAJA	(590)	RLHPETALKIMRNLAAILARRLVAANAKVDLLSAY
GLSA_ANASP	(335)	-----
Consensus	(601)	-----

GLSA\_CORGL : Q8NMT3; *Corynebacterium glutamicum*  
 GLSA\_COREF : Q8FMX4; *Corynebacterium efficiens*.  
 GLSA1\_BRAJA : Q89NA7; *Bradyrhizobium japonicum*,  
 GLSA2\_BRAJA : Q89KV2; *Bradyrhizobium japonicum*  
 GLSA\_ANASP : Q8YSZ5; *Anabaena* sp. (strain PCC 7120)